



SEQUENCE LISTING

<110> Madison, Edwin
Office of the President
Yeh, Juinn-Chern

<120> NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE 16, THE
ENCODED PROTEINS AND METHODS BASED THEREON

<130> 24745-1625

<140> 10/612,466

<141> 2003-07-01

<150> 60/394,347

<151> 2002-07-02

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3147

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (23)...(2589)

<223> Nucleotide sequence encoding MTSP1

<300>

<308> GenBank #AR081724

<309> 2000-08-31

<400> 1

tcaagagcgg cctcggggta cc	atg ggg agc gat cgg gcc cgc aag ggc gga	52
	Met Gly Ser Asp Arg Ala Arg Lys Gly Gly	
	1 5 10	
ggg ggc ccg aag gac ttc ggc gcg gga ctc aag tac aac tcc cgg cac		100
Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His		
	15 20 25	
gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac		148
Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn		
	30 35 40	
aac gtc aag aag gtg gaa aag cat ggc ccg ggg cgc tgg gtg gtg ctg		196
Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu		
	45 50 55	
gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc		244
Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe		
	60 65 70	
ctg gtg tgg cat ttg cag tac cgg gac gtg cgt gtc cag aag gtc ttc		292
Leu Val Trp His Leu Cln Tyr Arg Asp Val Arg Val Gln Lys Val Phe		
	75 80 85 90	

aat ggc tac atg agg atc aca aat gag aat ttt gtg gat gcc tac gag 340
 Asn Gly Tyr Met Arg Ile Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu
 95 100 105

aac tcc aac tcc act gag ttt gta agc ctg gcc agc aag gtg aag gac 388
 Asn Ser Asn Ser Thr Glu Phe Val Ser Leu Ala Ser Lys Val Lys Asp
 110 115 120

gcg ctg aag ctg ctg tac agc gga gtc cca ttc ctg ggc ccc tac cac 436
 Ala Leu Lys Leu Leu Tyr Ser Gly Val Pro Phe Leu Gly Pro Tyr His
 125 130 135

aag gag tcg gct gtg acg gcc ttc agc gag ggc agc gtc atc gcc tac 484
 Lys Glu Ser Ala Val Thr Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr
 140 145 150

tac tgg tct gag ttc agc atc ccg cag cac ctg gtg gag gag gcc gag 532
 Tyr Trp Ser Glu Phe Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu
 155 160 165 170

cgc gtc atg gcc gag gag cgc gta gtc atg ctg ccc ccg cgg gcg cgc 580
 Arg Val Met Ala Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg
 175 180 185

tcc ctg aag tcc ttt gtg gtc acc tca gtg gtg gct ttc ccc acg gac 628
 Ser Leu Lys Ser Phe Val Val Thr Ser Val Val Ala Phe Pro Thr Asp
 190 195 200

tcc aaa aca gta cag agg acc cag gac aac agc tgc agc ttt ggc ctg 676
 Ser Lys Thr Val Gln Arg Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu
 205 210 215

cac gcc cgc ggt gtg gag ctg atg cgc ttc acc acg ccc ggc ttc cct 724
 His Ala Arg Gly Val Glu Leu Met Arg Phe Thr Thr Pro Gly Phe Pro
 220 225 230

gac agc ccc tac ccc gct cat gcc cgc tgc cag tgg gcc ctg cgg ggg 772
 Asp Ser Pro Tyr Pro Ala His Ala Arg Cys Gln Trp Ala Leu Arg Gly
 235 240 245 250

gac gcc gac tca gtg ctg agc ctc acc ttc cgc agc ttt gac ctt gcg 820
 Asp Ala Asp Ser Val Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala
 255 260 265

tcc tgc gac gag cgc ggc agc gac ctg gtg acg gtg tac aac acc ctg 868
 Ser Cys Asp Glu Arg Gly Ser Asp Leu Val Thr Val Tyr Asn Thr Leu
 270 275 280

agc ccc atg gag ccc cac gcc ctg gtg cag ttg tgt ggc acc tac cct 916
 Ser Pro Met Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro
 285 290 295

ccc tcc tac aac ctg acc ttc cac tcc tcc cag aac gtc ctg ctc atc 964
 Pro Ser Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile
 300 305 310

aca ctg ata acc aac act gag cgg cgg cat ccc ggc ttt gag gcc acc 1012
 Thr Leu Ile Thr Asn Thr Glu Arg Arg His Pro Gly Phe Glu Ala Thr
 315 320 325 330

ttc ttc cag ctg cct agg atg agc agc tgt gga ggc cgc tta cgt aaa	1060
Phe Phe Gln Leu Pro Arg Met Ser Ser Cys Gly Gly Arg Leu Arg Lys	
335 340 345	
gcc cag ggg aca ttc aac agc ccc tac tac cca ggc cac tac cca ccc	1108
Ala Gln Gly Thr Phe Asn Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro	
350 355 360	
aac att gac tgc aca tgg aac att gag gtg ccc aac aac cag cat gtg	1156
Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val	
365 370 375	
aag gtg agc ttc aaa ttc ttc tac ctg ctg gag ccc ggc gtg cct gcg	1204
Lys Val Ser Phe Lys Phe Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala	
380 385 390	
ggc acc tgc ccc aag gac tac gtg gag atc aat ggg gag aaa tac tgc	1252
Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys	
395 400 405 410	
gga gag agg tcc cag ttc gtc gtc acc agc aac agc aac aag atc aca	1300
Gly Glu Arg Ser Gln Phe Val Val Thr Ser Asn Ser Asn Lys Ile Thr	
415 420 425	
gtt cgc ttc cac tca gat cag tcc tac acc gac acc ggc ttc tta gct	1348
Val Arg Phe His Ser Asp Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala	
430 435 440	
gaa tac ctc tcc tac gac tcc agt gac cca tgc ccg ggg cag ttc acg	1396
Glu Tyr Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr	
445 450 455	
tgc cgc acg ggg cgg tgt atc cgg aag gag ctg cgc tgt gat ggc tgg	1444
Cys Arg Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp	
460 465 470	
gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc	1492
Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala	
475 480 485 490	
ggc cac cag ttc acg tgc aag aac aag ttc tgc aag ccc ctc ttc tgg	1540
Gly His Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp	
495 500 505	
gtc tgc gac agt gtg aac gac tgc gga gac aac agc gac gag cag ggg	1588
Val Cys Asp Ser Val Asn Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly	
510 515 520	
tgc agt tgt ccg gcc cag acc ttc agg tgt tcc aat ggg aag tgc ctc	1636
Cys Ser Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu	
525 530 535	
tcg aaa agc cag cag tgc aat ggg aag gac gac tgt ggg gac ggg tcc	1684
Ser Lys Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser	
540 545 550	
gac gag gcc tcc tgc ccc aag gtg aac gtc gtc act tgt acc aaa cac	1732
Asp Glu Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His	
555 560 565 570	

acc tac cgc tgc ctc aat ggg ctc tgc ttg agc aag ggc aac cct gag	1780
Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu	
575 580 585	
tgt gac ggg aag gag gac tgt agc gac ggc tca gat gag aag gac tgc	1828
Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys	
590 595 600	
gac tgt ggg ctg cgg tca ttc acg aga cag gct cgt gtt gtt ggg ggc	1876
Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly	
605 610 615	
acg gat gcg gat gag ggc gag tgg ccc tgg cag gta agc ctg cat gct	1924
Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala	
620 625 630	
ctg ggc cag ggc cac atc tgc ggt gct tcc ctc atc tct ccc aac tgg	1972
Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp	
635 640 645 650	
ctg gtc tct gcc gca cac tgc tac atc gat gac aga gga ttc agg tac	2020
Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr	
655 660 665	
tca gac ccc acg cag tgg acg gcc ttc ctg ggc ttg cac gac cag agc	2068
Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser	
670 675 680	
cag cgc agc gcc cct ggg gtg cag gag cgc agg ctc aag cgc atc atc	2116
Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile	
685 690 695	
tcc cac ccc ttc ttc aat gac ttc acc ttc gac tat gac atc gcg ctg	2164
Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu	
700 705 710	
ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtg cgg ccc atc	2212
Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile	
715 720 725 730	
tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg	2260
Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp	
735 740 745	
gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc	2308
Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile	
750 755 760	
ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac	2356
Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn	
765 770 775	
ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtg ggc ttc ctc	2404
Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu	
780 785 790	
agc ggc ggc gtg gac tcc tgc cag ggt gat tcc ggg gga ccc ctg tcc	2452
Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser	
795 800 805 810	

agc gtg gag gcg gat ggg cgg atc ttc cag gcc ggt gtg gtg agc tgg 2500
 Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly Val Val Ser Trp
 815 820 825

gga gac ggc tgc gct cag agg aac aag cca ggc gtg tac aca agg ctc 2548
 Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu
 830 835 840

cct ctg ttt cgg gac tgg atc aaa gag aac act ggg gta ta ggggcccgggg 2599
 Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val
 845 850 855

ccacccaaat gtgtacacct gcgggggccac ccatcgctcca ccccagtgtg cagcctgca 2659
 ggctggagac tggaccgctg actgcaccag cgccccccaga acatacactg tgaactcaat 2719
 ctccagggct ccaaattctgc ctagaaaacc tctcgcttcc tcagcctcca aagtggagct 2779
 gggaggtaga aggggaggac actggtggtt ctactgacct aactgggggc aaaggtttga 2839
 agacacagcc tcccccgcca gcccgaagct gggccgaggc gcgtttgtgt atatctgcct 2899
 cccctgtctg taaggagcag cggaacgga gcttcggagc ctcctcagtg aaggtggtgg 2959
 ggctgccgga tctgggctgt ggggcccttg ggccacgctc ttgaggaagc ccaggctcgg 3019
 aggaccctgg aaaacagacg ggtctgagac tgaaattggt ttaccagctc ccagggtgga 3079
 cttcagtgtg tgtatttgtg taaatgggta aaacaattta tttcttttta aaaaaaaaaa 3139
 aaaaaaaaaa 3147

<210> 2
 <211> 855
 <212> PRT
 <213> Homo Sapien

<400> 2
 Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1 5 10 15
 Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
 20 25 30
 Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
 35 40 45
 Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
 50 55 60
 Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
 65 70 75 80
 Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
 85 90 95
 Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
 100 105 110
 Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
 115 120 125
 Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
 130 135 140
 Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
 145 150 155 160
 Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
 165 170 175
 Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
 180 185 190
 Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
 195 200 205
 Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
 210 215 220
 Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
 225 230 235 240
 His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu

245 250 255
 Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
 260 265 270
 Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
 275 280 285
 Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
 290 295 300
 Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
 305 310 315 320
 Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
 325 330 335
 Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
 340 345 350
 Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
 355 360 365
 Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Ser Phe Lys Phe
 370 375 380
 Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
 385 390 395 400
 Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
 405 410 415
 Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
 420 425 430
 Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
 435 440 445
 Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
 450 455 460
 Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
 465 470 475 480
 Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
 485 490 495
 Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
 500 505 510
 Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
 515 520 525
 Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
 530 535 540
 Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
 545 550 555 560
 Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
 565 570 575
 Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
 580 585 590
 Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
 595 600 605
 Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
 610 615 620
 Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
 625 630 635 640
 Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
 645 650 655
 Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
 660 665 670
 Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
 675 680 685
 Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
 690 695 700
 Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
 705 710 715 720
 Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser

tcgt gtt gtt ggg ggc acg gat gcg gat gag ggc gag tgg ccc tgg cag	1909
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln	
1 5 10 15	
gta agc ctg cat gct ctg ggc cag ggc cac atc tgc ggt gct tcc ctc	1957
Val Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu	
20 25 30	
atc tct ccc aac tgg ctg gtc tct gcc gca cac tgc tac atc gat gac	2005
Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp	
35 40 45	
aga gga ttc agg tac tca gac ccc acg cag tgg acg gcc ttc ctg ggc	2053
Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly	
50 55 60	
ttg cac gac cag agc cag cgc agc gcc cct ggg gtg cag gag cgc agg	2101
Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg	
65 70 75	
ctc aag cgc atc atc tcc cac ccc ttc ttc aat gac ttc acc ttc gac	2149
Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp	
80 85 90 95	
tat gac atc gcg ctg ctg gag ctg gag aaa ccg gca gag tac agc tcc	2197
Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser	
100 105 110	
atg gtg cgg ccc atc tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc	2245
Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala	
115 120 125	
ggc aag gcc atc tgg gtc acg ggc tgg gga cac acc cag tat gga ggc	2293
Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly	
130 135 140	
act ggc gcg ctg atc ctg caa aag ggt gag atc cgc gtc atc aac cag	2341
Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln	
145 150 155	
acc acc tgc gag aac ctc ctg ccg cag cag atc acg ccg cgc atg atg	2389
Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met	
160 165 170 175	
tgc gtg ggc ttc ctc agc ggc ggc gtg gac tcc tgc cag ggt gat tcc	2437
Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser	
180 185 190	
ggg gga ccc ctg tcc agc gtg gag gcg gat ggg cgg atc ttc cag gcc	2485
Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala	
195 200 205	
ggt gtg gtg agc tgg gga gac ggc tgc gct cag agg aac aag cca ggc	2533
Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly	
210 215 220	
gtg tac aca agg ctc cct ctg ttt cgg gac tgg atc aaa gag aac act	2581
Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr	
225 230 235	

ggg gta tag gggccggggc caccctaatg tgtacacctg cggggccacc
 Gly Val *
 240

2630

catcgtccac cccagtgtgc acgcctgcag gctggagact ggaccgctga ctgcaccagc 2690
 gccccagaa cataactgt gaactcaatc tccagggtc caaatctgcc tagaaaacct 2750
 ctcgcttct cagcctccaa agtggagctg ggaggtagaa ggggaggaca ctggtggttc 2810
 tactgaccca actgggggca aaggtttgaa gacacagcct ccccgccag cccaagctg 2870
 ggccgaggcg cgtttgtgta tatctgcctc ccctgtctgt aaggagcagc gggaacggag 2930
 cttcggagcc tcctcagtga agtggtggg gctgccggat ctgggctgtg gggcccttgg 2990
 gccacgctct tgaggaagcc caggctcggg ggaccctgga aaacagacgg gtctgagact 3050
 gaaattgttt taccagctcc cagggtggac ttcagtgtgt gtatttgtgt aaatgggtaa 3110
 aacaatttat ttctttttaa aaaaaaaaaa aaaaaaa 3147

<210> 4

<211> 241

<212> PRT

<213> Homo Sapien

<400> 4

Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1 5 10 15
 Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
 20 25 30
 Ser Pro Asn Trp Leu Val Ser Ala His Cys Tyr Ile Asp Asp Arg
 35 40 45
 Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
 50 55 60
 His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
 65 70 75 80
 Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
 85 90 95
 Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
 100 105 110
 Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
 115 120 125
 Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
 130 135 140
 Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
 145 150 155 160
 Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
 165 170 175
 Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
 180 185 190
 Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
 195 200 205
 Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
 210 215 220
 Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
 225 230 235 240
 Val

<210> 5

<211> 2293

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (2259)

<223> CVSP16 Full Length cDNA

```

<400> 5
atg gcc cgg cag ctg ctc ctc ccc ctt gtg gtg ctt gtc atc agt ccc 48
Met Ala Arg Gln Leu Leu Leu Pro Leu Val Val Leu Val Ile Ser Pro
1 5 10 15

atc cca gga gcc ttc cag gac tca gct ctc agt cct acc cag gaa gaa 96
Ile Pro Gly Ala Phe Gln Asp Ser Ala Leu Ser Pro Thr Gln Glu Glu
20 25 30

cct gaa gat ctg gac tgc ggg cgc cct gag ccc tcg gcc cgc atc gtg 144
Pro Glu Asp Leu Asp Cys Gly Arg Pro Glu Pro Ser Ala Arg Ile Val
35 40 45

ggg ggc tca aac gcg cag ccg ggc acc tgg cct tgg caa gtg agc ctg 192
Gly Gly Ser Asn Ala Gln Pro Gly Thr Trp Pro Trp Gln Val Ser Leu
50 55 60

cac cat gga ggt ggc cac atc tgc ggg ggc tcc ctc atc gcc ccc tcc 240
His His Gly Gly Gly His Ile Cys Gly Gly Ser Leu Ile Ala Pro Ser
65 70 75 80

tgg gtc ctc tcc gcc gct cac tgt ttc atg acg aat ggg acg ctg gag 288
Trp Val Leu Ser Ala Ala His Cys Phe Met Thr Asn Gly Thr Leu Glu
85 90 95

ccc gcg gcc gag tgg tcg gta ctg ctg ggc gtg cac tcc cag gac ggg 336
Pro Ala Ala Glu Trp Ser Val Leu Leu Gly Val His Ser Gln Asp Gly
100 105 110

ccc ctg gac ggc gcg cac acc cgc gca gtg gcc gcc atc gtg gtg ccg 384
Pro Leu Asp Gly Ala His Thr Arg Ala Val Ala Ala Ile Val Val Pro
115 120 125

gcc aac tac agc caa gtg gag ctg ggc gcc gac ctg gcc ctg ctg cgc 432
Ala Asn Tyr Ser Gln Val Glu Leu Gly Ala Asp Leu Ala Leu Leu Arg
130 135 140

ctg gcc tca ccc gcc agc ctg ggc ccc gcc gtg tgg cct gtc tgc ctg 480
Leu Ala Ser Pro Ala Ser Leu Gly Pro Ala Val Trp Pro Val Cys Leu
145 150 155 160

ccc cgc gcc tca cac cgc ttc gtg cac ggc acc gcc tgc tgg gcc acc 528
Pro Arg Ala Ser His Arg Phe Val His Gly Thr Ala Cys Trp Ala Thr
165 170 175

ggc tgg gga gac gtc cag gag gca gat cct ctg cct ctc ccc tgg gtg 576
Gly Trp Gly Asp Val Gln Glu Ala Asp Pro Leu Pro Leu Pro Trp Val
180 185 190

cta cag gaa gtg gag cta agg ctg ctg ggc gag gcc acc tgt caa tgt 624
Leu Gln Glu Val Glu Leu Arg Leu Leu Gly Glu Ala Thr Cys Gln Cys
195 200 205

ctc tac agc cag ccc ggt ccc ttc aac ctc act ctc cag ata ttg cca 672
Leu Tyr Ser Gln Pro Gly Pro Phe Asn Leu Thr Leu Gln Ile Leu Pro
210 215 220

ggg atg ctg tgt gct ggc tac cca ggg ggc cgc agg gac acc tgc cag 720

```

Gly Met Leu Cys Ala Gly Tyr Pro Gly Gly Arg Arg Asp Thr Cys Gln	
225 230 235 240	
ggg gac tct ggg ggg ccc ctg gtc tgt gag gaa ggc ggc cgc tgg ttc	768
Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Gly Gly Arg Trp Phe	
245 250 255	
cag gca gga atc acc agc ttt ggc ttt ggc tgt gga cgg aga aac cgc	816
Gln Ala Gly Ile Thr Ser Phe Gly Phe Gly Cys Gly Arg Arg Asn Arg	
260 265 270	
cct gga gtt ttc act gct gtg gct acc tat gag gca tgg ata cgg gag	864
Pro Gly Val Phe Thr Ala Val Ala Thr Tyr Glu Ala Trp Ile Arg Glu	
275 280 285	
cag gtg atg ggt tca gag cct ggg cct gcc ttt ccc acc cag ccc cag	912
Gln Val Met Gly Ser Glu Pro Gly Pro Ala Phe Pro Thr Gln Pro Gln	
290 295 300	
aag acc cag tca gat ccc cag gag ccc agg gag gag aac tgc acc att	960
Lys Thr Gln Ser Asp Pro Gln Glu Pro Arg Glu Glu Asn Cys Thr Ile	
305 310 315 320	
gcc ctg cct gag tgc ggg aag gcc ccg cgg cca ggg gcc tgg ccc tgg	1008
Ala Leu Pro Glu Cys Gly Lys Ala Pro Arg Pro Gly Ala Trp Pro Trp	
325 330 335	
gag gcc cag gtg atg gtg cca gga tcc aga ccc tgc cat ggg gcg ctg	1056
Glu Ala Gln Val Met Val Pro Gly Ser Arg Pro Cys His Gly Ala Leu	
340 345 350	
gtg tct gaa agc tgg gtc ttg gca cct gcc agc tgc ttt ctg gac ccg	1104
Val Ser Glu Ser Trp Val Leu Ala Pro Ala Ser Cys Phe Leu Asp Pro	
355 360 365	
aac agc tcc gac agc cca ccc cgc gac ctc gac gcc tgg cgc gtg ctg	1152
Asn Ser Ser Asp Ser Pro Pro Arg Asp Leu Asp Ala Trp Arg Val Leu	
370 375 380	
ctg ccc tcg cac ccg cgc gcg gag cgg gtg gcg cgc ctg gtg cag cac	1200
Leu Pro Ser His Pro Arg Ala Glu Arg Val Ala Arg Leu Val Gln His	
385 390 395 400	
gag aac gct tcg tgg gac aac gcc ccg gac ctg gcg ctg ctg cag ctg	1248
Glu Asn Ala Ser Trp Asp Asn Ala Pro Asp Leu Ala Leu Leu Gln Leu	
405 410 415	
cgc acg ccc gtg aac ctg agt gcg gct tcg cgg ccc gtg tgc cta ccc	1296
Arg Thr Pro Val Asn Leu Ser Ala Ala Ser Arg Pro Val Cys Leu Pro	
420 425 430	
cac ccg gaa cac tac ttc ctg ccc ggg agc cgc tgc cgc ctg gcc cgc	1344
His Pro Glu His Tyr Phe Leu Pro Gly Ser Arg Cys Arg Leu Ala Arg	
435 440 445	
tgg ggc cgc ggg gaa ccc gcg ctt ggc cca ggc gcg ctg ctg gag gcg	1392
Trp Gly Arg Gly Glu Pro Ala Leu Gly Pro Gly Ala Leu Leu Glu Ala	
450 455 460	
gag ctg tta ggc ggc tgg tgg tgc cac tgc ctg tac ggc cgc cag ggg	1440

Glu Leu Leu Gly Gly Trp Trp Cys His Cys Leu Tyr Gly Arg Gln Gly	
465 470 475 480	
gcg gca gta ccg ctg ccc gga gac ccg ccg cac gcg ctc tgc cct gcc	1488
Ala Ala Val Pro Leu Pro Gly Asp Pro Pro His Ala Leu Cys Pro Ala	
485 490 495	
tac cag gaa aag gag gag gtg ggc agc tgc tgg aat gac tgc cgt tgg	1536
Tyr Gln Glu Lys Glu Glu Val Gly Ser Cys Trp Asn Asp Ser Arg Trp	
500 505 510	
agc ctt ttg tgc cag gag gag ggg acc tgg ttt ctg gct gga atc aga	1584
Ser Leu Leu Cys Gln Glu Glu Gly Thr Trp Phe Leu Ala Gly Ile Arg	
515 520 525	
gac ttt ccc agt ggc tgt cta cgt ccc cga gcc ttc ttc cct ctg cag	1632
Asp Phe Pro Ser Gly Cys Leu Arg Pro Arg Ala Phe Phe Pro Leu Gln	
530 535 540	
act cat ggc cca tgg atc agc cat gtg act cgg gga gcc tac ctg gag	1680
Thr His Gly Pro Trp Ile Ser His Val Thr Arg Gly Ala Tyr Leu Glu	
545 550 555 560	
gac cag cta gcc tgg gac tgg ggc cct gat ggg gag gag act gag aca	1728
Asp Gln Leu Ala Trp Asp Trp Gly Pro Asp Gly Glu Glu Thr Glu Thr	
565 570 575	
cag act tgt ccc cca cac aca gag cat ggt gcc tgt ggc ctg cgg ctg	1776
Gln Thr Cys Pro Pro His Thr Glu His Gly Ala Cys Gly Leu Arg Leu	
580 585 590	
gag gct gct cca gtg ggg gtc ctg tgg ccc tgg ctg gca gag gtg cat	1824
Glu Ala Ala Pro Val Gly Val Leu Trp Pro Trp Leu Ala Glu Val His	
595 600 605	
gtg gct ggt gat cga gtc tgc act ggg atc ctc ctg gcc cca ggc tgg	1872
Val Ala Gly Asp Arg Val Cys Thr Gly Ile Leu Leu Ala Pro Gly Trp	
610 615 620	
gtc ctg gca gcc act cac tgt gtc ctc agg cca ggc tct aca aca gtg	1920
Val Leu Ala Ala Thr His Cys Val Leu Arg Pro Gly Ser Thr Thr Val	
625 630 635 640	
cct tac att gaa gtg tat ctg ggc cgg gca ggg gcc agc tcc ctc cca	1968
Pro Tyr Ile Glu Val Tyr Leu Gly Arg Ala Gly Ala Ser Ser Leu Pro	
645 650 655	
cag ggc cac cag atg acc tca gca ccg ccc ctc ctg tgc cag atg acg	2016
Gln Gly His Gln Met Thr Ser Ala Pro Pro Leu Leu Cys Gln Met Thr	
660 665 670	
gaa ggg tcc tgg atc ctc gtg ggc atg gct gtt caa ggg agc cgg gag	2064
Glu Gly Ser Trp Ile Leu Val Gly Met Ala Val Gln Gly Ser Arg Glu	
675 680 685	
ctg ttt gct gcc att ggt cct gaa gag gcc tgg atc tcc cag aca gtg	2112
Leu Phe Ala Ala Ile Gly Pro Glu Glu Ala Trp Ile Ser Gln Thr Val	
690 695 700	
gga gag gcc aac ttc ctg ccc ccc agt ggc tcc cca cac tgg ccc act	2160

Gly Glu Ala Asn Phe Leu Pro Pro Ser Gly Ser Pro His Trp Pro Thr
 705 710 715 720
 gga ggc agc aat ctc tgc ccc cca gaa ctg gcc aag gcc tcg gga tcc 2208
 Gly Gly Ser Asn Leu Cys Pro Pro Glu Leu Ala Lys Ala Ser Gly Ser
 725 730 735
 ccg cat gca gtc tac ttc ctg ctc ctg ctg act ctc ctg atc cag agc 2256
 Pro His Ala Val Tyr Phe Leu Leu Leu Leu Thr Leu Leu Ile Gln Ser
 740 745 750
 tga ggggctaggg tcccagcacc acttccccct tctc 2293
 *

<210> 6
 <211> 752
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CVSP16 Full Length Protein

<400> 6
 Met Ala Arg Gln Leu Leu Leu Pro Leu Val Val Leu Val Ile Ser Pro
 1 5 10 15
 Ile Pro Gly Ala Phe Gln Asp Ser Ala Leu Ser Pro Thr Gln Glu Glu
 20 25 30
 Pro Glu Asp Leu Asp Cys Gly Arg Pro Glu Pro Ser Ala Arg Ile Val
 35 40 45
 Gly Gly Ser Asn Ala Gln Pro Gly Thr Trp Pro Trp Gln Val Ser Leu
 50 55 60
 His His Gly Gly Gly His Ile Cys Gly Gly Ser Leu Ile Ala Pro Ser
 65 70 75 80
 Trp Val Leu Ser Ala Ala His Cys Phe Met Thr Asn Gly Thr Leu Glu
 85 90 95
 Pro Ala Ala Glu Trp Ser Val Leu Leu Gly Val His Ser Gln Asp Gly
 100 105 110
 Pro Leu Asp Gly Ala His Thr Arg Ala Val Ala Ala Ile Val Val Pro
 115 120 125
 Ala Asn Tyr Ser Gln Val Glu Leu Gly Ala Asp Leu Ala Leu Leu Arg
 130 135 140
 Leu Ala Ser Pro Ala Ser Leu Gly Pro Ala Val Trp Pro Val Cys Leu
 145 150 155 160
 Pro Arg Ala Ser His Arg Phe Val His Gly Thr Ala Cys Trp Ala Thr
 165 170 175
 Gly Trp Gly Asp Val Gln Glu Ala Asp Pro Leu Pro Leu Pro Trp Val
 180 185 190
 Leu Gln Glu Val Glu Leu Arg Leu Leu Gly Glu Ala Thr Cys Gln Cys
 195 200 205
 Leu Tyr Ser Gln Pro Gly Pro Phe Asn Leu Thr Leu Gln Ile Leu Pro
 210 215 220
 Gly Met Leu Cys Ala Gly Tyr Pro Gly Gly Arg Arg Asp Thr Cys Gln
 225 230 235 240
 Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Gly Gly Arg Trp Phe
 245 250 255
 Gln Ala Gly Ile Thr Ser Phe Gly Phe Gly Cys Gly Arg Arg Asn Arg
 260 265 270
 Pro Gly Val Phe Thr Ala Val Ala Thr Tyr Glu Ala Trp Ile Arg Glu

<210> 7
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 7
 ccctctgggt agccagcaca cagcatc 27

 <210> 8
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 8
 gccatcgtgg tgccggccaa ctacag 26

 <210> 9
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 9
 gcacacagca tccctggcaa tatctgg 27

 <210> 10
 <211> 26
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer

 <400> 10
 cggccaacta cagccaagtg gagctg 26

 <210> 11
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 11
 atggcccggc agctgctcct cccccttggtg 30

 <210> 12
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Primer

<400> 12
cggctcccgg gcaggaagta gtgttccg

28

<210> 13
<211> 9276
<212> DNA
<213> *Pichia pastoris*

<400> 13
agatctaaca tccaaagacg aaaggttgaa tgaaaccttt ttgccatccg acatccacag 60
gtccattctc acacataagt gccaaacgca acaggagggg atacactagc agcagaccgt 120
tgaaacgca ggacctccac tcctcttctc ctcaacaccc acttttgcca tcgaaaaacc 180
agcccagtta ttgggcttga ttggagctcg ctcatccaa ttccttctat taggctacta 240
acaccatgac tttattagcc tgtctatcct ggccccctg gcgagggttca tgtttgttta 300
tttcggaatg caacaagctc cgcattacac ccgaacatca ctccagatga gggctttctg 360
agtgtggggg caaatagttt catgttcccc aaatggccca aaactgacag tttaaacgct 420
gtcttgggaac ctaatatgac aaaagcgtga tctcatccaa gatgaactaa gtttggttcg 480
ttgaaatgct aacggccagt tgggtcaaaaa gaaacttcca aaagtcgcca taccgtttgt 540
cttgtttggg attgattgac gaatgctcaa aaataatctc attaatgctt agcgcagtct 600
ctctatcgct tctgaacccc ggtgcacctg tgccgaaacg caaatgggga aacacccgct 660
ttttggatga ttatgcattg tctccacatt gtatgcttcc aagattctgg tgggaatact 720
gctgatagcc taacgttcat gatcaaaatt taactgttct aacccctact tgacagcaat 780
atataaacag aaggaagctg ccctgtctta aacctttttt tttatcatca ttattagctt 840
actttcataa ttgcgactgg ttccaattga caagcttttg attttaacga cttttaacga 900
caacttgaga agatcaaaaa acaactaatt attcgaagga tccaaacgat gagatttcct 960
tcaattttta ctgcagtttt attcgcagca tcctccgcat tagctgctcc agtcaacact 1020
acaacagaag atgaaacggc acaaattccg gctgaagctg tcatcggtta ctcagattta 1080
gaaggggatt tcgatgttgc tgttttgcca ttttccaaca gcacaaataa cgggttattg 1140
tttataaata ctactattgc cagcattgct gctaaagaag aaggggtatc tctcgagaaa 1200
agagaggctg aagcttacgt agaattccct agggcgggcg cgaattaatt cgccttagac 1260
atgactgttc ctgagttcaa gttgggcact tacgagaaga ccggtcttgc tagattctaa 1320
tcaagaggat gtcagaatgc catttgccctg agagatgcag gcttcatttt tgatactttt 1380
ttatttgtaa cctatatagt ataggatttt ttttgtcatt ttgtttcttc tcgtacgagc 1440
ttgctcctga tcagcctatc tcgcagctga tgaatatctt cttcagagta cagaagatta 1500
tcattcgagt ttgatgtttt tcttgggtatt tcccactcct ataagcttta atgcggtagt ttatcacagt 1560
agtgagaagt tcgtttgtgc aagcttatcg gcaccgtgta tgaaatctaa caatgcgctc atcgatcacc 1620
taaattgcta acgcagtcag gcttcgctac gctgtaggca taggcttggt tatgccggta ctgccggggc 1680
tcggcaccgt caccctggat gctgtaggca tcgccagtca ctatggcggt ctgctagcgc 1740
tcttgcgagg tatcgtccat tccgacagca tcgccagtcg ccgttctcgg agcactgtcc gaccgctttg 1800
tatatgcgtt gatgcaattt ctatgcgcac ttggagccac tatcgactac gcgatcatgg 1860
gccgccgccc agtcctgctc gcttcgctac atctatcgaa tctaaatgta agttaaaatc tctaaataat 1920
cgaccacacc cgtcctgttg atctatcgaa ttaacagcat tgccggtgagc atctagacct 1980
taaataagtc ccagtttctc cactgcttgg ccaatatgtt tcagtccctc aggagttacg 2040
tcaacagcag ccagatccat ctggaaggtt gcagtgttaa ctccgctgta ttgacgggca 2100
tcttgtgaag tgatgaactt ctggaaaggt cccgaggagt aatctccaca actctctgga 2160
tatccgtacg ttggcaaaag gtgggttggt agatccagcg tgttgtactt gatcaacata agaagaagca 2220
gagtaggcac caacaaacac agatccagcg gtgttcagga gcgtagctat tggacatttc caaagcctgc 2280
ttctcgattt gcaggatcaa gtgttcagga gctgatgtgt cattttgaac catcatcttg 2340
tcgtagggtg caaccgatag ggttgtagag tgtgcaatac acttgcgtag aatttcaacc 2400
cttggcaact gcacagcttg gttgtgaaca gcatcttcaa ttctggcaag ctcttgtctt 2460
gtcatatcga cagccaacag aatcacctgg gaataatac catgttcagc ttgagacaga 2520
aggtctgagg caacgaaatc tggatcagcg tatttatcag caataactag aacttcagaa 2580
ggcccagcag gcatgtcaat actacacagg gctgatgtgt cacttttagg aacagtttct 2640
gcagcagtaa cgaactggtt tcctggacca aatatattgt cactttagg aacagtttct 2700
gttccgtaag ccatagcagc tactgcctgg gcgcctcctg ctagcacgat acacttagca 2760
ccaaccttgt gggcaacgta gatgacttct ggggtaaggg taccatcctt cttaggtgga 2820
gatgcaaaaa caatttcttt gcaaccagca actttggcag gaacaccag catcagggaa 2880

gtggaaggca	gaattgcggt	tccaccagga	atatagaggc	caactttctc	aataggtctt	2940
gcaaaacgag	agcagactac	accagggcaa	gtctcaactt	gcaacgtctc	cgttagttga	3000
gcttcatgga	atttcctgac	gttatctata	gagagatcaa	tggctctctt	aacgttatct	3060
ggcaattgca	taagtctctc	tgggaaagga	gcttctaaca	cagggtgtctt	caaagcgact	3120
ccatcaaact	tggcagttag	ttctaataagg	gctttgtcac	cattttgacg	aacattgtcg	3180
acaattgggt	tgactaattc	cataatctgt	tccgttttct	ggataggacg	acgaagggca	3240
tcttcaattt	cttgtgagga	ggccttagaa	acgtcaattt	tgcacaattc	aatacgacct	3300
tcagaaggga	cttcttttagg	tttggattct	tcttttaggt	gttccttggg	gtatcctggc	3360
ttggcatctc	ctttccttct	agtgcacttt	agggacttca	tatccaggtt	tctctccacc	3420
tcgtccaacg	tcacaccgta	cttggcacat	ctaactaatg	caaaataaaa	taagtcagca	3480
cattcccagg	ctatatcttc	cttggattta	gcttctgcaa	gttcatcagc	ttcctcccta	3540
atttttagcgt	tcaacaaaac	ttcgtcgtca	aataaccgtt	tgggtataaga	accttctgga	3600
gcattgctct	tacgatccca	caaggtggct	tccatggctc	taagaccctt	tgattggcca	3660
aaacaggaag	tgcgttccaa	gtgacagaaa	ccaacacctg	tttgttcaac	cacaaatttc	3720
aagcagtcct	catcacaatc	caattcgata	cccagcaact	tttgagttgc	tccagatgta	3780
gcacctttat	accacaaacc	gtgacgacga	gattggtaga	ctccagtttg	tgtccttata	3840
gcctccggaa	tagacttttt	ggacgagtac	accaggccca	acgagtaatt	agaagagtca	3900
gccaccaaa	tagtgaatag	accatcgggg	cggtcagtag	tcaaagacgc	caacaaaatt	3960
tcactgacag	ggaacttttt	gacatcttca	gaaagtctgt	attcagtagt	caattgcccga	4020
gcatcaataa	tggggattat	accagaagca	acaggtggaag	tcacatctac	caactttgcg	4080
gtctcagaaa	aagcataaac	agttctacta	ccgctacttag	tgaacttttt	caaatcgccc	4140
agtggagaag	aaaaaggcac	agcgatacta	gcattagcgg	gcaaggatgc	aactttatca	4200
accagggctc	tatagataac	cctagcgcct	gggatcatcc	tttggacaac	tctttctgcc	4260
aaatctaggt	ccaaaatcac	ttcattgata	ccattattgt	acaacttgag	caagttgtcg	4320
atcagctcct	caaattgggtc	ctctgtaacg	gatgactcaa	cttgcacatt	aacttgaagc	4380
tcagtcgatt	gagtgaactt	gatcagggtg	tgcagctggg	cagcagcata	gggaaacacg	4440
gcttttcccta	ccaaactcaa	ggaattatca	aactctgcaa	cacttgcgta	tgcaggtagc	4500
aagggaaatg	tcatacttga	agtcggacag	tgagtgtagt	cttgagaaat	tctgaagccg	4560
tatttttatt	atcagtgagt	cagtcatcag	gagatcctct	acgccggacg	catcgtggcc	4620
gacctgcagg	gggggggggg	gcgctgaggt	ctgcctcgtg	aagaagggtg	tgctgactca	4680
taccaggcct	gaatcgcccc	atcatccagc	cagaaagtga	gggagccacg	gttgatgaga	4740
gctttgttgt	aggtggacca	gttggtgatt	ttgaactttt	gctttgccac	ggaaacggtc	4800
gcgttgctcg	gaagatgcgt	gatctgatcc	ttcaactcag	caaaagtctg	atttattcaa	4860
caaagccgcc	gtccccgtcaa	gtcagcgtaa	tgctctgcca	gtgttacaac	caattaacca	4920
attctgatta	gaaaaactca	tcgagcatca	aatgaaactg	caattttatc	atatcaggat	4980
tatcaatacc	atatttttga	aaaagccgtt	tctgtaatga	aggagaaaaa	tcaccgaggc	5040
agttccatag	gatggcaaga	tcctggtatc	ggctcgcgat	tccgactcgt	ccaacatcaa	5100
tacaacctat	taatttcccc	tcgtcaaaaa	taaggttatc	aagtggagaaa	tcaccatgag	5160
tgacgactga	atccgggtgag	aatggcaaaa	gcttatgcat	ttctttccag	acttgttcaa	5220
caggccagcc	attacgctcg	tcataaaaat	cactcgcata	aaccaaaccg	ttattcattc	5280
gtgattgctc	ctgagcgaga	cgaaatacgc	gatcgcgtgt	aaaaggacaa	ttacaaacag	5340
gaatcgaaatg	caaccggcgc	aggaacactg	ccagcgcata	aacaataatt	tcacctgaat	5400
caggatattc	ttctaatacc	tggaaatgctg	ttttcccggg	gatcgcagtg	gtgagtaacc	5460
atgcatcatc	aggagtagcg	ataaaatgct	tgatggctcg	aagaggcata	aattccgtca	5520
gccagtttag	tctgaccatc	tcattctgtaa	catcattggc	aacgctacct	ttgccatggt	5580
tcagaaacaa	ctctggcgca	tcgggcttcc	catacaatcg	atagattgtc	gcacctgatt	5640
gccccgacatt	atcgcgagcc	catttatacc	catataaatc	agcatccatg	ttggaattta	5700
atcgcgccct	cgagcaagac	gtttcccgtt	gaatatggct	cataacaccc	cttgatttac	5760
tgtttatgta	agcagacagt	tttattgttc	atgatgatat	attttttatc	tgtgcaatgt	5820
aacatcagag	attttgagac	acaacgtggc	tttccccccc	ccccctgcag	gtcggcatca	5880
ccggcgccac	aggtgcgggt	gctggcgcc	atatcgccga	catcaccgat	ggggaagatc	5940
gggctcgcca	cttcgggctc	atgagcgctt	gtttcggcgt	gggtatgggtg	gcaggccccc	6000
tggccggggg	actgttgggc	gccatctcct	tgcatgcacc	attccttgcg	gcggcggtgc	6060
tcaacggcct	caacctacta	ctgggctgct	tcctaatagca	ggagtgcgat	aagggagagc	6120
gtcgagtatc	tatgattgga	agtatgggaa	tggtgatacc	cgcattcttc	agtgtcttga	6180
ggtctcctat	cagattatgc	ccaactaaag	caaccggagg	aggagatttc	atggtaaatt	6240
tctctgactt	ttggatcatc	gtagactcga	actgtgagac	tatctcgggt	atgacagcag	6300
aaatgtcctt	cttggagaca	gtaaatgaag	tcccaccaat	aaagaaatcc	ttgttatcag	6360
gaacaaactt	cttgtttcga	actttttcgg	tgccctgaac	tataaaatgt	agagtggata	6420
tgtcgggtag	gaatggagcg	ggcaaagtgt	taccttctgg	accttcaaga	ggtatgtagg	6480

gtttgtagat	actgatgcca	acttcagtga	caacgttgct	atttcggtca	aaccattccg	6540
aatccagaga	aatcaaagtt	gtttgtctac	tattgatcca	agccagtgcg	gtcttgaaac	6600
tgacaatagt	gtgctcgtgt	tttgagggtca	tcttttgtag	aataaatcta	gtctttgatc	6660
taaataatct	tgacgagcca	aggcgataaa	tacccaaatc	taaaactctt	ttaaaacgtt	6720
aaaaggacaa	gtatgtctgc	ctgtattaaa	ccccaaatca	gctcgtagtc	tgatcctcat	6780
caacttgagg	ggcactatct	tggttttagag	aaatttgcg	agatgcgata	tcgagaaaaa	6840
ggtacgctga	ttttaaacgt	gaaatttatc	tcaagatctc	tgcctcgcgc	gtttcgggtga	6900
tgacgggtgaa	aacctctgac	acatgcagct	cccggagacg	gtcacagctt	gtctgtaagc	6960
ggatgccggg	agcagacaag	cccgtcaggg	cgcgtcagcg	ggtgttgggc	ggtgtcgggg	7020
cgcagccatg	acccagtcac	gtagcgatag	cggagtgtat	actggcttaa	ctatgcggca	7080
tcagagcaga	ttgtactgag	agtgcaccat	atgcgggtgtg	aaataccgca	cagatgcgta	7140
aggagaaaat	accgcatcag	gcgctcttcc	gcttcctcgc	tcactgactc	gctgcgctcg	7200
gtcgttcggc	tcgggcgagc	ggtatcagct	cactcaaagg	cggtaataacg	gttatccaca	7260
gaatcagggg	ataacgcagg	aaagaacatg	tgagcaaaag	gccagcaaaa	ggccaggaac	7320
cgtaaaaagg	ccgcgttgct	ggcgtttttc	cataggctcc	gccccctga	cgagcatcac	7380
aaaaatcgac	gctcaagtca	gaggtggcga	aacccgacag	gactataaag	ataccaggcg	7440
tttccccctg	gaagctccct	cgtgcgctct	cctgtttccga	ccctgccgct	taccggatac	7500
ctgtccgcct	ttctcccttc	gggaagcgtg	gcgctttctc	aatgctcacg	ctgtagggtat	7560
ctcagttcgg	tgtaggctcg	tcgctccaag	ctgggctgtg	tgacgaacc	ccccgttcag	7620
cccgaccgct	gcgccttatc	cggtaactat	cgtcttgagt	ccaaccgggt	aagacacgac	7680
ttatcgccac	tggcagcagc	cactggtaac	aggattagca	gagcgaggta	tgtaggcggt	7740
gctacagagt	tcttgaagtg	gtggcctaac	tacggctaca	ctagaaggac	agtatttggt	7800
atctgcgctc	tgctgaagcc	agttaccttc	ggaaaaagag	ttggtagctc	ttgatccggc	7860
aaacaaacca	ccgctggtag	cggtgggtttt	tttgtttgca	agcagcagat	tacgcgcaga	7920
aaaaaaggat	ctcaagaaga	tcctttgatc	ttttctacgg	ggtctgacgc	tcagtggaac	7980
gaaaactcac	gttaagggat	tttgggtcatg	agattatcaa	aaaggatctt	cactagatc	8040
cttttaaat	aaaaatgaag	ttttaaatca	atctaagta	tatatgagta	aacttggtct	8100
gacagttacc	aatgcttaat	cagtgaaggca	cctatctcag	cgatctgtct	atttcggtca	8160
tccatagttg	cctgactccc	cgtcgtgtag	ataactacga	tacgggaggg	cttaccatct	8220
ggccccagtg	ctgcaatgat	accgcgagac	ccacgctcac	cggctccaga	tttatcagca	8280
ataaaccagc	cagccggaag	ggccgagcgc	agaagtgggtc	ctgcaacttt	atccgcctcc	8340
atccagtcta	ttaattgttg	ccgggaagct	agagtaagta	gttcgccagt	taatagtttg	8400
cgcaacggtg	ttgccatttg	tgcaggcatc	gtgggtgtcac	gctcgtcgtt	tggtatggct	8460
tcattcagct	ccggttccca	acgatcaagg	cgagttacat	gatcccccat	gttgtgcaaa	8520
aaagcgggtta	gctccttcgg	tcctccgatc	gttgtcagaa	gtaagtgggc	cgcagtgtta	8580
tcactcatgg	ttatggcagc	actgcataat	tctcttactg	tcatgccatc	cgtaagatgc	8640
ttttctgtga	ctggtgagta	ctcaaccaag	tcattctgag	aatagtgtat	gcggcgaccg	8700
agttgtctct	gcccggcgctc	aacacgggat	aataccgcgc	cacatagcag	aactttaaaa	8760
gtgctcatca	ttggaaaacg	ttcttcgggg	cgaaaactct	caaggatctt	accgctgttg	8820
agatccagtt	cgatgtaacc	cactcgtgca	cccaactgat	cttcagcatc	ttttactttc	8880
accagcgttt	ctgggtgagc	aaaaacagga	aggcaaaatg	ccgcaaaaaa	gggaataagg	8940
gcgacacgga	aatggtgaat	actcatactc	ttcctttttc	aatattattg	aagcatttat	9000
cagggttatt	gtctcatgag	cggatacata	tttgaatgta	tttagaaaaa	taaacaaata	9060
gggggtccgc	gcacatttcc	ccgaaaagtg	ccacctgacg	tctaagaaac	cattattatc	9120
atgacattaa	cctataaaaa	taggcgtatc	acgaggccct	ttcgtcttca	agaattaatt	9180
ctcatgtttg	acagcttatc	atcgataagc	tgactcatgt	tggtattgtg	aaatagacgc	9240
agatcgggaa	cactgaaaaa	taacagttat	tattcgc			9276

<210> 14
 <211> 11
 <212> PRT
 <213> Pichia pastoris

<400> 14
 Lys Arg Ile Ala Ser Gly Val Ile Ala Pro Lys
 1 5 10

<210> 15
 <211> 30
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 15

tgggtcttgg cacctgccag ctgctttctg

30

<210> 16

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 16

gaagggggaa gtggtgctgg gaccctag

28

<210> 17

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 17

ccctctgggt agccagcaca cagcatc

27

<210> 18

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 18

gccatcgtgg tgccggccaa ctacag

26

<210> 19

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 19

atcgtggtgc cggccaacta cagccaagtg

30

<210> 20

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 20
 acccatcacc tgctcccgta tccatgcctc

30

<210> 21
 <211> 103
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Polypeptide

<400> 21
 Val Ser Arg Leu Val Ile Ser Ile Arg Leu Pro Gln His Leu Gly Leu
 1 5 10 15
 Arg Pro Pro Leu Ala Leu Leu Glu Leu Ser Ser Arg Val Glu Pro Ser
 20 25 30
 Pro Ser Ala Leu Pro Ile Cys Leu His Pro Ala Gly Ile Pro Pro Gly
 35 40 45
 Ala Ser Cys Trp Val Leu Gly Trp Lys Glu Pro Gln Asp Arg Val Pro
 50 55 60
 Val Ala Ala Ala Val Ser Ile Leu Thr Gln Arg Ile Cys Asp Cys Leu
 65 70 75 80
 Tyr Gln Gly Ile Leu Pro Pro Gly Thr Leu Cys Val Leu Tyr Ala Glu
 85 90 95
 Gly Gln Glu Asn Arg Cys Glu
 100

<210> 22
 <211> 37
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Polypeptide

<400> 22
 Asn Asp Ser Arg Trp Ser Leu Leu Cys Gln Glu Glu Gly Thr Trp Phe
 1 5 10 15
 Leu Ala Gly Ile Arg Asp Phe Pro Ser Gly Cys Leu Arg Pro Arg Ala
 20 25 30
 Phe Phe Pro Leu Gln
 35